

STIC-Biotech/ChemLib

87441

From: Hutzell, Paula
Sent: Tuesday, February 25, 2003 4:20 PM
To: Collins, Cynthia; STIC-Biotech/ChemLib
Subject: RE: RUSH interference sequence search request SN 09/846903

Approved

-----Original Message-----

From: Collins, Cynthia
Sent: Tuesday, February 25, 2003 4:18 PM
To: Hutzell, Paula
Subject: RUSH interference sequence search request SN 09/846903

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

Paula,

Can you approve and forward this rush sequence search request? It is for an amended case.

Please search, both prior art and interference, for SN 09/846903:

1) SEQ ID NO:79

Thank You,

Cynthia Collins
Art Unit 1638
CM1, 9A12 (office) or 9E12 (mailbox)
(703) 605-1210

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

TYPE OF SEARCH:

VENDOR/COST (Agency, fee, etc.)

Date Picked up: _____
Date Completed: 3/10/03
Searcher Prep/Review: _____
Clerical: _____

Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____

Register Office: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____



11017 APR 89 54 AM '89
JOURNAL : W : 01879 A 79 08 MAY 1989

Monsanto Technology LLC (US)

ATTRIBUTES

501174

Figure 1

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/ob xref "Taxon:4577"

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11/15/2011 11:45 AM

BASE CATALYST 4.95 g 4.92 g

NOTES

Query Match

	Socially responsible	100.0%	Score = 78.69	Pearson's chi-square
	Best local similarity	100.0%	Prod. No.	($\chi^2_{(1)}=10.54; p<.01$)

Best local similarity 100.0%; Prec. No. 0; Matches 223; Conservative 0; Mismatches

1	CTCTGCTCTTGCGGCAATTCGTGTAATCTACCTGACAGATTAAGATTTCTGTCGGGCTCATCGGT	60
1	CTCTGCTCTTGCGGCAATTCGTGTAATCTACCTGACAGATTAAGATTTCTGTCGGGCTCATCGGT	60
61	AGGCAAAATCTGCTTATTGCACTCTTAAGAGGTAGACATAATCAACTCCCTACTATGACACC	120
61	AGGCAAAATCTGCTTATTGCACTCTTAAGAGGTAGACATAATCAACTCCCTACTATGACACC	120
121	TATGTAGGTATCTGTGAGTAGAGGAAATGATCTTACACIAAGAGCTGATTCAGAGCAAGATTA	180
121	TATGTAGGTATCTGTGAGTAGAGGAAATGATCTTACACIAAGAGCTGATTCAGAGCAAGATTA	180
181	ACTCTTCAAGTGTGCTTAATAAATAATACCTTTGGAGCAAGATTAATTTGGCAATTGTTAG	240
181	ACTCTTCAAGTGTGCTTAATAAATAATACCTTTGGAGCAAGATTAATTTGGCAATTGTTAG	240
241	GTGAAGGTACTTAATGTGATTTGGGCTCACTCTTCAGAGCACTTTTATACTCGAAATATGCA	300
241	GTGAAGGTACTTAATGTGATTTGGGCTCACTCTTCAGAGCACTTTTATACTCGAAATATGCA	300
301	CATCAAGCTACAGAGTATTAATAATCTTTGAGAGCAAGATTAATTTGGCAATTGTTAG	360
301	CATCAAGCTACAGAGTATTAATAATCTTTGAGAGCAAGATTAATTTGGCAATTGTTAG	360
361	GATTAAATCTTGAAGTCAACGCTTTTACTCTAAATCTATGATCTCTTCTTAAGCAAGC	420
361	GATTAAATCTTGAAGTCAACGCTTTTACTCTAAATCTATGATCTCTTCTTAAGCAAGC	420
421	TTTAGAAGCTGTGTTTTGGAGCTTTGTAATTTGGGCTCTCAAGTTATTAATTTTGTGAATC	480
421	TTTAGAAGCTGTGTTTTGGAGCTTTGTAATTTGGGCTCTCAAGTTATTAATTTTGTGAATC	480
481	TAACTCTTTTGTCAAGAAAAAATACTCATATATGCAATGGGTACCTTTGGGGAGCTTCTA	540
481	TAACTCTTTTGTCAAGAAAAAATACTCATATATGCAATGGGTACCTTTGGGGAGCTTCTA	540
541	TTCTCAACATCATCTGCTTTAACTTTTACTTTGACACAAAGCTAGTGTGCTTTTCAGGAATAT	600
541	TTCTCAACATCATCTGCTTTAACTTTTACTTTGACACAAAGCTAGTGTGCTTTTCAGGAATAT	600
601	CTCTACTGATGTACAGAAAGCAAGCTTCGGGTGAGTAAGGGATTCAGAGCAAGCATTTGCAT	660
601	CTCTACTGATGTACAGAAAGCAAGCTTCGGGTGAGTAAGGGATTCAGAGCAAGCATTTGCAT	660
661	CAAAAGCTCAAGAGCTATTAATCAAGTTGATAGTTTCGATGACACAAAGGAGTTCACAG	720
661	CAAAAGCTCAAGAGCTATTAATCAAGTTGATAGTTTCGATGACACAAAGGAGTTCACAG	720
721	TACAGGTCAAAAGAAAAAGCAAGCAAGGCTTAAATGCGAGCAAGTGGCAAGATTTGCAAAAT	780
721	TACAGGTCAAAAGAAAAAGCAAGCAAGGCTTAAATGCGAGCAAGTGGCAAGATTTGCAAAAT	780
781	AGCTACTCTGCTTAAACACATTTGTAAGCAACTGCAAGGCTTAATTCGTAATTTATCTACTAA	840
781	AGCTACTCTGCTTAAACACATTTGTAAGCAACTGCAAGGCTTAATTCGTAATTTATCTACTAA	840
841	CTGGGCTGCTGTCGGCTCTAAATACAGATGAACAGTAAACCGGTATAAATTTACATTTTGGCAG	900
841	CTGGGCTGCTGTCGGCTCTAAATACAGATGAACAGTAAACCGGTATAAATTTACATTTTGGCAG	900

[illegible]

(http://cbl.ceh.ac.uk/ncb/ncbi/ncblast-dbl) and the cDNA sequence database at NCBI. Protein homologies of the coding regions were searched against NCBI Nonredundant protein database with BLAST2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding NCBI accession no. and gene clone ID. A gene with identity of significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the whole length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from the M13 promoter of the BAC clone. This sequence of RU108H10 clone has an overlap with B1075066 (bbaA_49032) clone at the position 1 to 14,667 of 5' end and overlaps with R300306(A90472) at the position of 133,526 to the 357 of 5' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://www.doe.arizona.edu/genomes/Ses>.

FEATURES	Location/Qualifiers
SOURCE	136357

1. 13837
/organism: "Oriza sativa (arroz) cultivar-grupo"

"Ja equoq; in" - exiitque

/s/ John A. Nippobare
/s/ Alex - "Iaxo-39947"

$$n = \frac{1}{\sqrt{\pi}} \ln \left(\frac{1 + \sqrt{1 - \pi}}{1 - \sqrt{1 - \pi}} \right)$$

Clone "B1108H10"

	JOHN(324)	3539	3508	3666	4238	4548	4589.
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4745. .4758)

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/proc "B108H10.1"

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join(324) 3533.3
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4745, 4758)

/qene- "B1108H1C

[illegible][illegible]

7428. 8396

/qene- "B1108H10.2"

7428. 8396

"2.01H801IN" - check/

/note "probably inactive due to no termination codon in

CDS

probably in

anobondene

Similar to

opend/

Join(9310. 9551, 9

/join/9310 9551 9

JOINT 0156)M10F

note="contains" style="display: none;">

ZHOU, CONG-LIN ESIS
C71859(E046A) 072648(P2001) 98611(E046A)

similar to *Oryza sativa* chromosome 1, P0493G01.14
C1639 (30464) 72720+8 (1207) 333661 (P0487)

unknown protein"

/codon_start-1

/protein_id="BA842720.1"

"050802 13m 10x-96/"

* "MV" = MV₀M; other cases are MV₀L, MV₀S, etc.

SMVHCRAPOCEVAEISPRGSLGSPCLVYKGVIMIQERIA^{THC}"

join(13008. 13165

15996. .16158, 2015.

/gene - "BI108H10.4"

join(13008	13165	13238	13306	14712	14850	15804
15006	15159	20154	20286			

15996. .16158, 20
20000 - 16158, 20

gene	<p>/codon_start=1</p> <p>/db_xref="GI:20802721.1"</p> <p>/translation="MAEITFAAGSGVILKILVIAREKFEVITDFRIQHLIRGGQGVNLVPSMFLNCCGATSVKWLQCVVSVASVITPCEIPLWLFNVEVHEIVAFETPNCXVPMELKPMFNGVILILHKQANCVETSTFAHMACDQGNNGNVAEVSPEAGETMDAGITTSKSSVANDKSLVLEASGCVGQVQVHPATILTNNGDQPEVEHIVIASQHPYILSMELLFAMPNASGHELAWGTUVSTIENHHGFTTHVFCTESTSEKVEYIEHPAHLIFAKELLAMKTLILIDIMPTAVNNS"</p> <p>join(3107..32155,22451..22202,22551..22202,22514..22739,23798..24160)</p> <p>/gene="B1108H10.5"</p> <p>join(21137..21155,21151..21202,22551..22571,23614..23739,23798..24160)</p> <p>/gene="B1108H10.5"</p> <p>/note="hypothetical protein similar to <i>Crypta salina</i> chromosome 10, G2JNP4002902.1"</p> <p>/codon_start=1</p> <p>/protein_id="BAP92723.1"</p> <p>/db_xref="GI:20805048"</p>
LTR	<p>/translation="MQLERDDEKWESEFRVILRSQQSLIPKIRKARLEPKYKIVTVSTITVAPINANFETILINRPNWSSCYVAHVNVIVDPKPSVAVFEITTHWFFQRTSLISPTPMVAATVFATHEFPQKRSPIISQDMEVAVFEITTHWFFQKRSPIISRTPFVAVFEITTHWFKNTQITWFENQKRSPIISPTPMFVVV"</p> <p>complement(21910..22638)</p> <p>/note="3' LTR"</p>
gene	<p>complement(25912..31005)</p> <p>/gene="B1108H10.6"</p> <p>complement(25912..31005)</p> <p>/gene="B1108H10.6"</p> <p>/note="probably inactive due to stop codon(s) in CDS pseudogene similar to <i>Crypta salina</i> chromosome 1, P04P0A01.2"</p> <p>/pseudo</p>
gene	<p>complement(32316..35736)</p> <p>/gene="B1108H10.7"</p> <p>complement(32316..35736)</p> <p>/gene="B1108H10.7"</p>
misc_feature	<p>/note="TNP live transposable element probably inactive due to frameshift(s) in CDS probably inactive due to no termination codon in CDS pseudogene"</p> <p>/pseudo</p>
LTR	<p>complement(36659..437386)</p> <p>/note="5' LTR"</p>
gene	<p>join(38213..38361,40249..40441)</p> <p>/gene="B1108H10.8"</p>
CDS	<p>join(38213..38361,40249..40441)</p> <p>/gene="B1108H10.8"</p> <p>/note "contains EST AC092422(550524) unknown protein"</p> <p>/codon_start=1</p> <p>/protein_id="BAP92723.1"</p> <p>/db_xref="GI:20805049"</p>
misc_feature	<p>/translation="MAEAGSGVKKHLLAREKDVAFERIDILIRGAGLVDPVPSMKAPHWGTEVSIENHGGFTVFESTFESTSEKVEYIEHPAIVETANFFLPIVLEKTLIDYKPTIVNNS"</p> <p>join(41759..42560)</p> <p>/note="5' LTR"</p>
LTR	<p>43777..48553</p> <p>/gene="B1108H10.9"</p>
gene	<p>43777..48553</p> <p>/gene="B1108H10.9"</p> <p>/note="probably inactive due to stop codon(s) in CDS pseudogene, gag-pol polyprotein"</p> <p>/pseudo</p>
LTR	<p>48457..49360</p> <p>/note="3' LTR"</p>
gene	<p>complement(50166..50519)</p> <p>/gene="B1108H10.10"</p>
CDS	<p>complement(join(50166..50300,50370..50519))</p> <p>/gene="B1108H10.10"</p> <p>/note="hypothetical protein"</p>

male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen tolerance -

Claim 1: page 104-106; 121pp; English.

The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, fragments, deletions or sub-elements of the sequences, are capable of regulating transcription of an operably linked DNA sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as anthers, especially wheat anthers and as such, for regulating transcription of a DNA sequence, by operably linking the DNA sequence to the promoter. The promoter sequences are useful in plants to regulate transcription of target genes including genes for control of fertility, insect or pathogen resistance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAG5584-AAG5587 represent the corn promoter sequences of the present invention.

Sequence 2213 BP; 656 A; 496 C; 492 G; 569 T; () other;

Query Match	100.0%	Score 2213	DB 24	Length 2213
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2213	Conservative	0	Mismatches 0	Indels 0
				Gaps 0

QY	1	CTCTGCTTGGATATTTCTGAGCTACTCTGAGAGATTAAGTCTTTCTGCTCCGCTCATCGGT	60
DB	1	TT	60
QY	61	AGGTAATCTGTCTATTGCACTCTAAAGAGCTAGAGATAATCAATTAACAAATCCGCTAGTGCAC	120
DB	61	TT	120
QY	121	TATGTAGGCGATATTTGAGTACAGAGCGAATTAATCTTTATTAAGACGTGATTCAGGCTAAAGTTA	180
DB	121	TATGTAGGCGATATTTGAGTACAGAGCGAATTAATCTTTATTAAGACGTGATTCAGGCTAAAGTTA	180
QY	181	ATCTCTGAAGCTGTCTCTTAACAAATAACTTTTGGATTAAGCTTGAATTTTGGCAATTCGTAG	240
DB	181	ATCTCTGAAGCTGTCTCTTAACAAATAACTTTTGGATTAAGCTTGAATTTTGGCAATTCGTAG	240
QY	241	GTGAAGCGATTAATATGATCTGCGCTCAAGCTCTTCAGGCACTTTTATCTGAAAATGCA	300
DB	241	GTGAAGCGATTAATATGATCTGCGCTCAAGCTCTTCAGGCACTTTTATCTGAAAATGCA	300
QY	361	TATTAAGCGATATGAGTCATGAGAAATATGTTCTGCTATGAGTCTGAAAGTCCGCTGCTGAT	360
DB	361	TATTAAGCGATATGAGTCATGAGAAATATGTTCTGCTATGAGTCTGAAAGTCCGCTGCTGAT	360
QY	361	CAATTAACCTTCTAGCTCAAGCTTTTATTTTCAAAATCATCAAGCTCTTCTTTAAACAAGC	420
DB	361	CAATTAACCTTCTAGCTCAAGCTTTTATTTTCAAAATCATCAAGCTCTTCTTTAAACAAGC	420
QY	421	TTTAGAAGTTGTTTCTTGGATCTTTGGAAATTTGGGCTCTCAAGTATTAATTTTTCGAATC	480
DB	421	TTTAGAAGTTGTTTCTTGGATCTTTGGAAATTTGGGCTCTCAAGTATTAATTTTTCGAATC	480
QY	481	TAAATCTCTTGGCAAGCAAAACAACTCATATCGCAATAGGCTTACTTTTGGGCACTTCTTA	540
DB	481	TAAATCTCTTGGCAAGCAAAACAACTCATATCGCAATAGGCTTACTTTTGGGCACTTCTTA	540
QY	541	TGTTGAAGATCACTTGTCTTAAACTTTTACTTTTTCATCAAAAGCTAGCTTTTCAGCAATAT	600
DB	541	TGTTGAAGATCACTTGTCTTAAACTTTTACTTTTTCATCAAAAGCTAGCTTTTCAGCAATAT	600
QY	661	CTTATATGATGAGAAGGGAAGCTTGGGCTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT	660
DB	661	CTTATATGATGAGAAGGGAAGCTTGGGCTGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT	660

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XX Sequence 294 BP; 79 A; 85 C; 46 G; 36 T; 6 other;
 SQ Best Local Similarity 85.6%; Pred. No. 9; 4e-09;
 Query Match 4.0%; Score 65.4; DB 24; Length 293;
 Matches 84; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 2117 AGGCATCTTACGACAAATCTGACGCTTACGCTGGGAGGAGAGCCACGATCTTCA 2176
 DQ 132 AGGCATCTTACGACAAATCTGACGCTTACGCTGGGAGGAGAGCCACGATCTTCA 190
 QY 2177 TCCGCAAGGCGGACGACGCTTGGTGGGCGGCTGCTCACTT 2213
 DQ 191 TCCGCAAGGCGGACGACGCTTGGTGGGCGGCTGCTCACTT 227

RESULT 9
 ABL75058
 XX ABL74770 standard; cDNA; 64 BP;
 AC ABL74770;
 XX 14-MAY-2002 (first entry)
 XX corn tassel-derived polynucleotide (cdps) SEQ ID No:4144;
 XX Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;
 KW inheritance; characteristic; growth; development; disease resistance;
 KW environmental adaptability; quality; yield; molecular marker;
 KW multigene trait; plant breeding; corn tassel; gene; ss.
 OS Zea mays.
 XX US2001051345-A1.
 XX 13-DEC-2001.
 XX 16-APR-1999; 990S-0294094.
 XX 21-APR-1998; 980S-082567P.
 XX (LALG/) LALGHD1 R V.
 PA (ITOL/) ITO L Y.
 PA (SHER/) SHERMAN R K.
 XX Lalquid RV, Ito LY, Sherman RK;
 XX WPI; 2002 16364721.
 XX Novel purified corn tassel derived polynucleotide useful for
 PI determining altered gene expression, to recover regulatory elements and
 PI to follow inheritance of desirable characteristics through hybrid
 PI breeding programs
 XX Claim 1: SEQ ID 4144; 201pp; English.
 XX The present sequence describes a purified corn tassel-derived
 CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
 CC selected from those given in ABL746627 to ABL746833, the cdps sequences
 CC encode corn tassel derived polypeptides (CDPS). The cdps sequences (1)
 CC can be used for determining altered gene expression, to recover
 CC regulatory elements and to follow inheritance of desirable
 CC characteristics through hybrid breeding programs. (1) are also useful
 CC in the evaluation, and alteration of desired characteristics associated
 CC with growth and development, disease resistance, environmental
 CC adaptability, quality and yield, and as molecular markers for studying
 CC inheritance of multigene traits in a plant breeding program. (1) can be
 CC used to produce a tassel specific profile of gene transcription, a
 CC transcript image, to clone regulatory elements for use in transformation
 CC vectors, to express a polypeptide, to identify, isolate or extend
 CC identical or related corn tassel nucleic acid sequences from DNA
 CC libraries, in nucleic acid hybridisation or amplification technologies,
 CC as query sequences to determine homology of known sequences, as probe

CC for use in Southern or Northern hybridisation, and to identify the
 CC presence of and/or to determine the degree of similarity between two
 CC (or more) nucleic acid sequences.
 XX Sequence 64 BP; 21 A; 18 C; 16 G; 8 T; 1 other;
 SQ Query Match 2.8%; Score 62; DB 24; Length 64;
 Best Local Similarity 98.4%; Pred. No. 4e-08;
 Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1761 TGTATGCGGCAATGCGGCAAGGAGAGAGAGAAATAGTAAAGGGAATGCTGCTTCA 1820
 DQ 2 TGTATGCGGCAATGCGGCAAGGAGAGAGAAATAGTAAAGGGAATGCTGCTTCA 64
 QY 1821 AAA 1823
 DQ 62 AAA 64

RESULT 10
 ABL75058
 XX ABL75058 standard; cDNA; 299 BP;
 AC ABL75058;
 XX 14-MAY-2002 (first entry)
 XX Corn tassel derived polynucleotide (cdps) SEQ ID No:4432;
 XX Corn; corn tassel derived polynucleotide; cdps; hybrid breeding; CDPS;
 KW inheritance; characteristic; growth; development; disease resistance;
 KW environmental adaptability; quality; yield; molecular marker;
 KW multigene trait; plant breeding; corn tassel; gene; ss.
 OS Zea mays.
 XX US2001051345-A1.
 XX 13-DEC-2001.
 XX 16-APR-1999; 990S-0294094.
 XX 21-APR-1998; 980S-082567P.
 XX (LALG/) LALGHD1 R V.
 PA (ITOL/) ITO L Y.
 PA (SHER/) SHERMAN R K.
 XX Lalquid RV, Ito LY, Sherman RK;
 XX WPI; 2002 16364721.
 XX Novel purified corn tassel derived polynucleotide useful for
 PI determining altered gene expression, to recover regulatory elements and
 PI to follow inheritance of desirable characteristics through hybrid
 PI breeding programs
 XX Claim 1: SEQ ID 4432; 201pp; English.
 XX The present sequence describes a purified corn tassel derived
 CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
 CC selected from those given in ABL746627 to ABL746833, the cdps sequences
 CC encode corn tassel derived polypeptides (CDPS). The cdps sequences (1)
 CC can be used for determining altered gene expression, to recover
 CC regulatory elements and to follow inheritance of desirable
 CC characteristics through hybrid breeding programs. (1) are also useful
 CC in the evaluation, and alteration of desired characteristics associated
 CC with growth and development, disease resistance, environmental
 CC adaptability, quality and yield, and as molecular markers for studying
 CC inheritance of multigene traits in a plant breeding program. (1) can be
 CC used to produce a tassel specific profile of gene transcription, a
 CC transcript image, to clone regulatory elements for use in transformation
 CC vectors, to express a polypeptide, to identify, isolate or extend
 CC identical or related corn tassel nucleic acid sequences from DNA
 CC libraries, in nucleic acid hybridisation or amplification technologies,
 CC as query sequences to determine homology of known sequences, as probe


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Best Local Similarity: 5.0%; Seed: No. 0.0076;
Matches: 14; Conservative: 157; Mismatches: 108; Indels: 0; Gaps: 0;

QY 642 GGGAAAGGCTGACAGAAAGCAATGACATGAAAGAGTGAAGAGTATTAACCAAAAGTTGAT 691
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1420 KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1261

QY 692 AATTCATGACACAAAGCAATGCTTCAATATGAAAGAGAAAGAAAGAGAGAGAGCT 751
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1420 KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1291

QY 752 AATTCATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1420 KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1341

QY 812 TGAGAGGCTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 871
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1140 KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1091

QY 872 AGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1080 KRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1042

RESULT 2
US-09-135-994 1
Sequence 1, Application US/09135994A
Patent No. 6280946
GENERAL INFORMATION:
APPLICANT: BODUM ET AL.
TITLE OF INVENTION: 37A7 GENE AND METHOD OF USE
FILE REFERENCE: UNIVERSITY OF MINNESOTA
CURRENT APPLICATION NUMBER: US/99/135,994A
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 56/056,179
EARLIER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 477
TYPE: DNA
ORGANISM: Homo sapiens
US-09-135-994-1

Query Match
Best Local Similarity: 52.6%; Seed: No. 0.011;
Matches: 90; Conservative: 0; Mismatches: 44; Indels: 0; Gaps: 0;

QY 1864 GGGGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1923
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 174 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 234

QY 1924 GGTGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1983
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 234 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203

QY 1984 AGCTTACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 294 TGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 346

RESULT 3
US-09-253-691-3
Sequence 3, Application US/99253691
Patent No. 6124100
GENERAL INFORMATION:
APPLICANT: Dong Kyu Jin
TITLE OF INVENTION: Diagnostic Method and Kit for Neuropsychiatric Diseases
FILE REFERENCE: 1942/36
CURRENT APPLICATION NUMBER: US/99/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278

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EARLIER FILING DATE: 1996-02-26
NUMBER OF SEQ ID NOS: 3
SOFTWARE: WordPerfect 6.1/Windows
SEQ ID NO 3
LENGTH: 397
TYPE: DNA
ORGANISM: human
US-09-253-691-3

Query Match
Best Local Similarity: 55.4%; Seed: No. 0.013;
Matches: 77; Conservative: 0; Mismatches: 62; Indels: 0; Gaps: 0;

QY 1264 GGTGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1923
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 250 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309

QY 1924 GGTGAGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1983
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 310 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 369

QY 1984 AGCTTACATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2002
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 370 ACAGAGTTCACATCCATGT 488

RESULT 4
US-09-117-121-27
Sequence 27, Application US/99117121
Patent No. 6407020
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Geng, Zhiguan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4844
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPIER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 97/27497/00062
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/INCKET NUMBER: 016252-00161005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 34..153
OTHER INFORMATION: /product "SAFE7 (S9)"

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,094
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 43,229
; REFERENCE/SEQUENCE NUMBER: 729,124,2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-4100
; TELEFAX: (215) 568-4449
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
; PCT US94-04496-29

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Query Match 1.7%, Score 47.4; DB 3; Length 3376;
Best Local Similarity 53.8%; Pred. No. 0.36;
Matches 77; Conservative 0; Mismatches 66; Indels 6; Gaps 0;

QY 1834 AGGTGCTCTTACGGTAATGCTTCTATGCGGCTACGACAGGAGAAAGGACTGTA 1893
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 605 AGACAGAGAGGAGCCGACCAAGAGAGATGATATAGAGGAGGAGGAGGAGGAGTA 664

QY 1894 GTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1953
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 665 GTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 724

QY 1954 GCGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1976
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Gb 725 GCAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747

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RESULT 7
PCT US94-04496-29
; Sequence 29, Application US/09574942
; GENERAL INFORMATION:
; APPLICANT: Crocco, Carlo
; APPLICANT: Gaudini, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics, and Methods
; TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: us-09-846-903-79
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 43,229
; REFERENCE/SEQUENCE NUMBER: 129-124,2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-4100
; TELEFAX: (215) 568-4449

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; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
; PCT US94-04496-29

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Query Match 1.7%, Score 47.4; DB 3; Length 4376;
Best Local Similarity 53.8%; Pred. No. 0.40;
Matches 77; Conservative 0; Mismatches 66; Indels 6; Gaps 0;

QY 1834 AGGTGCTCTTACGGTAATGCTTCTATGCGGCTACGACAGGAGAAAGGACTGTA 1893
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 605 AGACAGAGAGGAGCCGACCAAGAGAGATGATATAGAGGAGGAGGAGGAGGAGTA 664

QY 1894 GTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1953
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 665 GTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 724

QY 1954 GCGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1976
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Gb 725 GCAGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747

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RESULT 8
US-09-574-942-1
; Sequence 1, Application US/09574942
; Patent No. 6,458,724
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan K.
; APPLICANT: Krieser, Ronald J.
; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND GENES
; FILE REFERENCE: DE-0137
; CURRENT APPLICATION NUMBER: 09/574,942
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/541,840
; PCT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Mus sp.
; US-09-574-942-1

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Query Match 1.7%, Score 46.8; DB 4; Length 1224;
Best Local Similarity 56.7%; Pred. No. 0.47;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 392 CAAATGATACAGCTCTCTTTAAACAAGCTTTAGGAAATGTTTTCGAGCTTGAAT 451
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 525 CAGCTGCAATACCTTCGGATACAGGCCAGCTTTGAGGAAATAGATTTTCAGCTCTGCTT 584

QY 452 TCGAGCTCCAACTTATAATTTTTCGAATCTAAGCTCTTCCAAAAGAAATTAAT 511
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Gb 585 ACAAATCAATCATACAGCTATCTTCAATCAAGTAATTTTCATGGAATTAATTAAT 644

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RESULT 9
US-08-998-416-915
; Sequence 915, Application US/08998416
; Patent No. 6,239,264
; GENERAL INFORMATION:
; APPLICANT: Phillipsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen

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181 GAAAGAGAACCGACATAAAATACATTTGGCAGGAGTGTACAGCTTTGTATAGCTCAGGCT 240
928 CCAAAACACATTCGTCTATTTGGACATAGAAAGTCAATGTAATGATGATTGTAACTTGTGT 987
241 CCAAAACACATTCGTCTATTTGGACATAGAAAGTCAATGTAATGATGATTGTAACTTGTGT 300
988 TCTATACACATAAATGAAATCTTAAGGACATAGACATGAGTCTTCATATCTTCGTCATGTT 1047
401 TCTATACAGAAATGAAATCTTAAGGACATAGACATGAGTCTTCATATCTTCGTCATGTT 360
1048 TTTAGTATCTAGTCTGATTATATCCAACTTCGTCTCTGATGATGATATATATCCCAAGAGCT 1107
461 TTTAGTATCTAGTCTGATTATATCCAACTTCGTCTCTGATGATGATATATATCCCAAGAGCT 420
1108 AACATCTAAGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 1167
421 AACATCTAAGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 480
1168 TTTAGCAATTAAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 1227
481 TTTAGCAATTAAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 540
1228 AAATTCAGCAAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 1287
541 AAATTCAGCAAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 600
1288 CATCTCTTCAAAAAGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 1347
601 CATCTCTTCAAAAAGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 660
1348 CCAAAATTCGCTAATGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 1407
661 CCAAAATTCGCTAATGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTGTCTTTTATTTC 720
1408 GAATTTTATGCTAATACCTTTTACAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1467
721 GAATTTTATGCTAATACCTTTTACAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 780
1468 TTGCAATACAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1527
781 TTGCAATACAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 840
1528 TTTTAAAGCAAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1587
841 TTTTAAAGCAAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 900
1588 AGCAATACAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1647
901 AGCAATACAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 960
1648 AGGAGGAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1707
961 AGGAGGAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1020
1708 CATAGCAAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1767
1021 CATAGCAAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1080
1768 CCAATACAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1793
1081 CCAATACAGGAGGAGGAGGAGGAGGCTTCTAGCTTTTAAACATGCTGTGTCTTTTATTTC 1104

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RESULT 2

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US-09-894-633A-94
: Sequence: 94, Application: US/09/04/04/04
: Patent No.: US20010051345A1
: GENERAL INFORMATION:

```

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: APPLICANT: Conner, Timothy
: APPLICANT: Dubois, Patricia
: APPLICANT: Malvern, Marianne
: APPLICANT: Masurel, James

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: TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRE
: FILE REFERENCE: 38-21(15856)B
: CURRENT APPLICATION NUMBER: US/09/894/633A
: PRIOR FILING DATE: 2001-06-28
: PRIOR APPLICATION NUMBER: 60/214,357
: PRIOR FILING DATE: 2000-06-28
: PRIOR APPLICATION NUMBER: 09/894,633
: PRIOR FILING DATE: 2000-06-28
: NUMBER OF SEQ ID NOS: 111
: SOFTWARE: Patent In version 3.0
: SEQ ID NO: 94
: LENGTH: 721
: TYPE: DNA
: ORGANISM: Zea mays
: US-09-894-633A-94

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Query Match 4.0%; Score 88; DB 10; Length 721;
Best Local Similarity 73.6%; Pred. No. 1,86-14;
Matches 156; Conservative 0; Mismatches 45; Indels 11; Gaps 4;

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QY 1598 CTTTGAACCGGAGAGTGTCTCA---ATGACCTATATAAAAGGAGGAAATAGGAGTGTG 1654
DB 512 CTTTGAACCGGAGAGTGTCTCA---ATGACCTATATAAAAGGAGGAAATAGGAGTGTG 571
QY 1655 CTTTGAACCGGAGAGTGTCTCA---ATGACCTATATAAAAGGAGGAAATAGGAGTGTG 1714
DB 572 CTTTGAACCGGAGAGTGTCTCA---ATGACCTATATAAAAGGAGGAAATAGGAGTGTG 641
QY 1715 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1774
DB 632 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 684
QY 1775 CCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1806
DB 684 CCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715

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RESULT 3

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US-09-294-093B-6185
: Sequence: 6185, Application: US/09/294/093B
: Patent No.: US20010051345A1
: GENERAL INFORMATION:

```

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: APPLICANT: Lalqui, Raghunath, V.
: APPLICANT: Ito, Laura, Y.
: APPLICANT: Sherman, Bradley, K.
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
: FILE REFERENCE: 01-0009 US

```

```

: CURRENT APPLICATION NUMBER: US/09/294/093B
: PRIOR FILING DATE: 1999-04-16
: PRIOR APPLICATION NUMBER: 02/082,567
: PRIOR FILING DATE: April 21, 1998

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: NUMBER OF SEQ ID NOS: 6207
: SOFTWARE: PERL Program
: SEQ ID NO: 6185

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: LENGTH: 283
: TYPE: DNA

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: ORGANISM: Zea mays
: FEATURE:

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: NAME/KEY: misc-feature
: OTHER INFORMATION: Inycle 10 No. US20010051345A1 700384159H1

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: NAME/KEY: unsure
: LOCATION: 77, 250

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: OTHER INFORMATION: a, b, c, d, or other
: US-09-294-093B-6185

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Query Match 3.1%; Score 69.4; DB 10; Length 283;
Best Local Similarity 60.2%; Pred. No. 1,66-09;
Matches 171; Conservative 0; Mismatches 77; Indels 34; Gaps 4;

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QY 1758 CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1817
DB 1 CATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60

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